

EXPRESS MAIL NO. EV719382212US



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

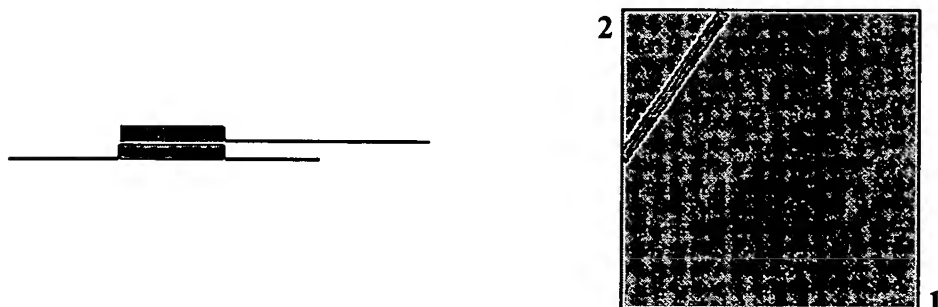
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix ☒ BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ View option ☒ Standard
Masking character option ☒ X for protein, n for nucleotide Masking color option ☒ Black
☐ Show CDS translation ☒ Align

Sequence 1: lcl|1_seq_WNV20
Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_JEV
Length = 111 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 97.8 bits (242), Expect = 2e-19
Identities = 42/54 (77%), Positives = 51/54 (94%), Gaps = 0/54 (0%)

Query	1	TPVGRLVTVPFVSVATANSKVLIELEPPFSDSYIVVGRGEQQINHHWHKSGSS	54
		TPVGRLVTVPFV+ ++ANSKVL+E+EPPF DSYIVVG G++QINHHWHK+GS+	
Sbjct	58	TPVGRLVTVPFVATSSANSKVLVEMEPFGDSYIVVGMGDKQINHHWHKAGST	111

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda	K	H
0.322	0.137	0.417

Gapped		
Lambda	K	H
0.267	0.0410	0.140



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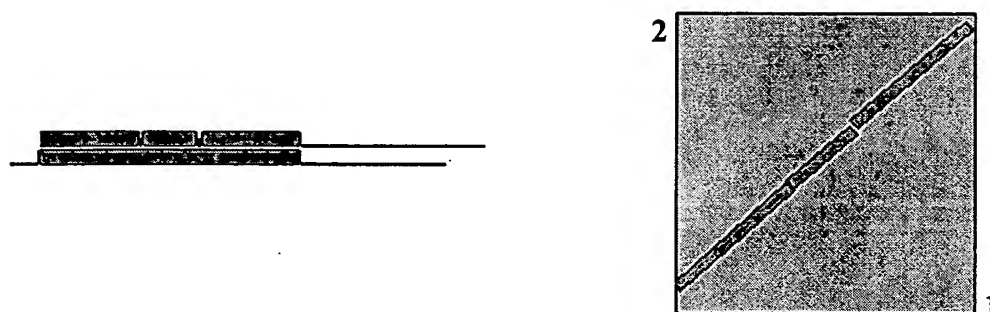
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|1_seq_Dengue
Length = 94 (1 .. 160)

Sequence 2: lcl|2_seq_JEV
Length = 111 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 91.3 bits (225), Expect = 1e-17
Identities = 41/96 (42%), Positives = 61/96 (63%), Gaps = 3/96 (3%)

Query	1	MCSGKFSIDKEMAETQHGTTVVKVKEYEGAGAPCKVPI-EIRDVNKEKVVGRIISSTPL--	57
		MC+ KFS K A+T HGT V+++ Y G+ PCK+PI + +N VGR+++ P	
Sbjct	12	MCTEKFSFAKNPADTGHGTVVIELSYSGSDGPCKIPIVSVASLNDMTVPVGRVTVNPFVA	71
Query	58	AENTNSVTNIELEPPFGDSYIVIGVGN SALT LHWFR	93
		+ NS +E+EPFGDSYIV+G+G+ + HW +	
Sbjct	72	TSSANSKVLVEMEPPFGDSYIVVGMGDKQINHHWHK	107

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H
0.315 0.133 0.390



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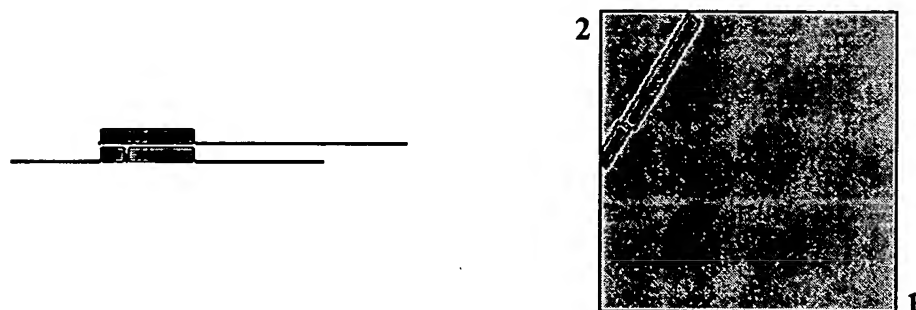
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix ☒ BLOSUM62 ☒ gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ View option ☒
 Masking character option ☒ X for protein, n for nucleotide ☒ Masking color option ☒
☐ Show CDS translation

Sequence 1: lcl|1_seq_WNV20
 Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_dengue
 Length = 94 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 47.4 bits (111), Expect = 2e-04
 Identities = 22/48 (45%), Positives = 28/48 (58%), Gaps = 2/48 (4%)

```
Query 3  VGR LVT VNP FSV VAT ANSKV LIE LPP FSD SYIV VGR GEQQ INHH WHK 50
          VGR+++ P      NS  IELEPPF DSYIV+G G  + HW +
Sbjct 48  VGR IISSTPLAE--NTNSVTNIELEPPFGDSYIVIGVGN SALT LHWFR 93
```

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
 0.322 0.137 0.417

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 104
Number of extensions: 63
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 72 (32.3 bits)

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 90

Number of extensions: 42

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 94

Length of database: 1,357,962,904

Length adjustment: 69

Effective length of query: 25

Effective length of database: 1,357,962,835

Effective search space: 33949070875

Effective search space used: 33949070875

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (22.0 bits)

S2: 71 (32.0 bits)

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 135
Number of extensions: 65
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 72 (32.3 bits)